

SEQUENCE LISTING

<110> KWEE, YONG
KOSAKA, MASA AKI
KOISHIHARA, YASUO

<120> HM1.24-UTILIZING CANCER VACCINES

<130> 053466-0401

<140> 10/533,104

<141> 2005-04-28

<150> PCT/JP03/13954

<151> 2003-10-30

<150> JP 2002-316639

<151> 2002-10-30

<160> 23

<170> PatentIn Ver. 3.3

<210> 1

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
comprising leader sequence and HA coding sequence

<400> 1

aattccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60
ccactcatat ccatacgacg tccagacta cgctggtacc gcggccgcg 109

<210> 2

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
comprising leader sequence and HA coding sequence

<400> 2

gatccgcggc cgcggtacca gcgtagtctg ggacgtcgta tgggtatgag tggacacctg 60
tagctgttgc taccaagaag aggatgatac agtccatcc catggtggg 109

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 3

taaaggtacc aacagcgagg cctgccg

27

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4

ctgctgcagt gagatcccag gatccata

28

<210> 5

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(396)

<220>

<223> Nucleotide sequence of extracellular domain of soluble HM 1.24 antigenic protein

<400> 5

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| aac | agc | gag | gcc | tgc | cgg | gac | ggc | ctt | cgg | gca | gtg | atg | gag | tgt | cgc | 48 |
| Asn | Ser | Glu | Ala | Cys | Arg | Asp | Gly | Leu | Arg | Ala | Val | Met | Glu | Cys | Arg | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| aat | gtc | acc | cat | ctc | ctg | caa | caa | gag | ctg | acc | gag | gcc | cag | aag | ggc | 96 |
| Asn | Val | Thr | His | Leu | Leu | Gln | Gln | Glu | Leu | Thr | Glu | Ala | Gln | Lys | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttt | cag | gat | gtg | gag | gcc | cag | gcc | gcc | acc | tgc | aac | cac | act | gtg | atg | 144 |
| Phe | Gln | Asp | Val | Glu | Ala | Gln | Ala | Ala | Thr | Cys | Asn | His | Thr | Val | Met | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | cta | atg | gct | tcc | ctg | gat | gca | gag | aag | gcc | caa | gga | caa | aag | aaa | 192 |
| Ala | Leu | Met | Ala | Ser | Leu | Asp | Ala | Glu | Lys | Ala | Gln | Gly | Gln | Lys | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | gag | gag | ctt | gag | gga | gag | atc | act | aca | tta | aac | cat | aag | ctt | cag | 240 |
| Val | Glu | Glu | Leu | Glu | Gly | Glu | Ile | Thr | Thr | Leu | Asn | His | Lys | Leu | Gln | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gac | gcg | tct | gca | gag | gtg | gag | cga | ctg | aga | aga | gaa | aac | cag | gtc | tta | 288 |
| Asp | Ala | Ser | Ala | Glu | Val | Glu | Arg | Leu | Arg | Arg | Glu | Asn | Gln | Val | Leu | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |

agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 384
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 115 120 125

gct ctg ctg cag 396
Ala Leu Leu Gln
130

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<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 6
ataggatcct caagcggagc tggagtcctg 30

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<210> 7
<211> 345
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) .. (345)
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<220>
<223> Nucleotide sequence of extracellular domain of
C-terminal lacking soluble HM 1.24 antigenic
protein

<400> 7
aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc 48
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
1 5 10 15

aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
20 25 30

ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
35 40 45

gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
50 55 60

gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 240
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80

gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95

agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110

agc tcc gct 345
 Ser Ser Ala
 115

<210> 8
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 8
 ggatcttggt tcattctcaa gcctcagaca gt 32

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 9
 cctcagactc ggctgaccc gtggaaagaa 30

<210> 10
 <211> 429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence coding for a fusion protein
 comprising HA peptide and soluble HM 1.24
 antigenic protein

<220>

<221> CDS

<222> (1)..(429)

<400> 10

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tac | cca | tac | gac | gtc | cca | gac | tac | gct | ggg | acc | aac | agc | gag | gcc | tgc | 48 |
| Tyr | Pro | Tyr | Asp | Val | Pro | Asp | Tyr | Ala | Gly | Thr | Asn | Ser | Glu | Ala | Cys | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| cgg | gac | ggc | ctt | cgg | gca | gtg | atg | gag | tgt | cgc | aat | gtc | acc | cat | ctc | 96 |
| Arg | Asp | Gly | Leu | Arg | Ala | Val | Met | Glu | Cys | Arg | Asn | Val | Thr | His | Leu | |
| | | 20 | | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| ctg | caa | caa | gag | ctg | acc | gag | gcc | cag | aag | ggc | ttt | cag | gat | gtg | gag | 144 |
| Leu | Gln | Gln | Glu | Leu | Thr | Glu | Ala | Gln | Lys | Gly | Phe | Gln | Asp | Val | Glu | |
| | | 35 | | | | | 40 | | | | | | 45 | | | |
| | | | | | | | | | | | | | | | | |
| gcc | cag | gcc | gcc | acc | tgc | aac | cac | act | gtg | atg | gcc | cta | atg | gct | tcc | 192 |
| Ala | Gln | Ala | Ala | Thr | Cys | Asn | His | Thr | Val | Met | Ala | Leu | Met | Ala | Ser | |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| | | | | | | | | | | | | | | | | |
| ctg | gat | gca | gag | aag | gcc | caa | gga | caa | aag | aaa | gtg | gag | gag | ctt | gag | 240 |
| Leu | Asp | Ala | Glu | Lys | Ala | Gln | Gly | Gln | Lys | Lys | Val | Glu | Glu | Leu | Glu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| | | | | | | | | | | | | | | | | |
| gga | gag | atc | act | aca | tta | aac | cat | aag | ctt | cag | gac | gcg | tct | gca | gag | 288 |
| Gly | Glu | Ile | Thr | Thr | Leu | Asn | His | Lys | Leu | Gln | Asp | Ala | Ser | Ala | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| | | | | | | | | | | | | | | | | |
| gtg | gag | cga | ctg | aga | aga | gaa | aac | cag | gtc | tta | agc | gtg | aga | atc | gcg | 336 |
| Val | Glu | Arg | Leu | Arg | Arg | Glu | Asn | Gln | Val | Leu | Ser | Val | Arg | Ile | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| | | | | | | | | | | | | | | | | |
| gac | aag | aag | tac | tac | ccc | agc | tcc | cag | gac | tcc | agc | tcc | gct | gcg | gcg | 384 |
| Asp | Lys | Lys | Tyr | Tyr | Pro | Ser | Ser | Gln | Asp | Ser | Ser | Ser | Ala | Ala | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| | | | | | | | | | | | | | | | | |
| ccc | cag | ctg | ctg | att | gtg | ctg | ctg | ggc | ctc | agc | gct | ctg | ctg | cag | | 429 |
| Pro | Gln | Leu | Leu | Ile | Val | Leu | Leu | Gly | Leu | Ser | Ala | Leu | Leu | Gln | | |
| | | 130 | | | | | 135 | | | | 140 | | | | | |

<210> 11

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence coding for a fusion protein
comprising HA peptide and C-terminal lacking
soluble HM 1.24 antigenic protein

<220>

<221> CDS

<222> (1)..(378)

```

<400> 11
tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc 48
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
  1              5              10              15

cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc 96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
      20              25              30

ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag 144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
      35              40              45

gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc 192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
      50              55              60

ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag 240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
      65              70              75              80

gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag 288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
      85              90              95

gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg 336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
      100              105              110

gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct 378
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
      115              120              125

```

```

<210> 12
<211> 379
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence coding for L chain V region
      version a of humanized anti-HM 1.24 antibody

```

```

<220>
<221> CDS
<222> (1)..(378)

```

```

<220>
<221> sig_peptide
<222> (1)..(57)

```

```

<220>
<221> mat_peptide
<222> (58)..(378)

```

```

<400> 12
atg gga tgg agc tgt atc atc ctc tcc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-15 -10 -5

gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
15 20 25

aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40 45

ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 240
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
50 55 60

ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
80 85 90

act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c 379
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

```

```

<210> 13
<211> 418
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence coding for H chain V region
version r of humanized anti-HM 1.24 antibody

```

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<220>
<221> CDS
<222> (1)..(417)

```

```

<220>
<221> sig_peptide
<222> (1)..(57)

```

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<220>
<221> mat_peptide
<222> (58)..(417)

```

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<400> 13
atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
          -15                      -10                      -5

gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
          -1  1                      5                      10

cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          15                      20                      25

act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          30                      35                      40                      45

gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
          50                      55                      60

cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288
Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
          65                      70                      75

aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
          80                      85                      90

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
          95                      100                      105

tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418
Trp Gly Gln Gly Thr Val Thr Val Ser Ser
110                      115                      120

```

```

<210> 14
<211> 418
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence coding for H chain V region
      version s of humanized anti-HM 1.24 antibody

```

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<220>
<221> CDS
<222> (1)..(417)

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<220>
<221> sig_peptide
<222> (1)..(57)

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<220>

<221> mat_peptide

<222> (58)..(417)

<400> 14

| | |
|-----------------------------------------------------------------|-----|
| atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt | 48 |
| Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly | |
| -15 -10 -5 | |
| | |
| gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag | 96 |
| Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys | |
| -1 1 5 10 | |
| | |
| cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc | 144 |
| Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe | |
| 15 20 25 | |
| | |
| act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt | 192 |
| Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu | |
| 30 35 40 45 | |
| | |
| gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt | 240 |
| Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser | |
| 50 55 60 | |
| | |
| cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc | 288 |
| Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser | |
| 65 70 75 | |
| | |
| aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg | 336 |
| Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val | |
| 80 85 90 | |
| | |
| tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac | 384 |
| Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr | |
| 95 100 105 | |
| | |
| tgg ggg caa ggg acc acg gtc acc gtc tcc tca g | 418 |
| Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser | |
| 110 115 120 | |

<210> 15

<211> 1014

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotide sequence coding for human HM 1.24
antigenic protein expressed on cell membrane

<220>

<221> CDS

<222> (23)..(562)

<400> 15

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gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc aga 52
                        Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg
                        1                      5                      10

gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg ata 100
Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile
                        15                      20                      25

gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg att 148
Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile
                        30                      35                      40

atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt cgg 196
Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg
                        45                      50                      55

gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg 244
Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu
                        60                      65                      70

acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc 292
Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr
                        75                      80                      85                      90

tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag 340
Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys
                        95                      100                      105

gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca 388
Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr
                        110                      115                      120

tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga 436
Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg
                        125                      130                      135

aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac 484
Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr
                        140                      145                      150

ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg att 532
Pro Ser Ser Gln Asp Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile
                        155                      160                      165                      170

gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 582
Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
                        175                      180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 642

ttctgagcgg gtcattggggc aacacggtta gcggggagag cacggggtag ccggagaagg 702

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 762

ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtcct ccctcttgct 822

tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tggtgttatg 882

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ggttttttttt gcggggggggg ttgctttttt ctggggtctt tgagctccaa aaaaataaac 942
 acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaattc 1002
 gggcggccgc ca 1014

<210> 16
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence of soluble HM 1.24
 antigenic protein

<400> 16
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 1 5 10 15
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 20 25 30
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 35 40 45
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 50 55 60
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110
 Ser Ser Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 115 120 125
 Ala Leu Leu Gln
 130

<210> 17
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence of extracellular downing of
 C-terminal lacking soluble HM 1.24 antigenic
 protein

<400> 17

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 1 5 10 15

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 20 25 30

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 35 40 45

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 50 55 60

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110

Ser Ser Ala
 115

<210> 18

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of a fusion protein
 comprising HA peptide and soluble HM 1.24
 antigenic protein

<400> 18

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15

Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30

Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45

Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60

Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80

Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95

Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala
 115 120 125

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
 130 135 140

<210> 19

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of a fusion protein
 comprising HA peptide and C-terminal lacking
 soluble HM 1.24 antigenic protein

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15

Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30

Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45

Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60

Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80

Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95

Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
 115 120 125

<210> 20

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of L chain V region
 version a of humanized anti-HM 1.24 antibody

<400> 20

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
 -15 -10 -5

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120

<210> 22
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
amino acid sequence of H chain V region
version s of humanized anti-HM 1.24 antibody

<400> 22
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1 5 10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
50 55 60
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
65 70 75
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
95 100 105
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120

<210> 23
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence of human HM 1.24
antigenic protein expressed on cell membrane

<400> 23
Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1 5 10 15
Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
 180